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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09/155,514	11/17/98	KAINOH	1102-98

HM12/0615
SCHNADER HARRISON SEGAL & LEWIS
1600 MARKET STREET
36TH FLOOR
PHILADELPHIA PA 19103

EXAMINER
SCHWADRON, R

ART UNIT	PAPER NUMBER
1644	11

DATE MAILED: 06/15/00

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks



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SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER	
ART UNIT	PAPER NUMBER

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application
Commissioner of Patents

The communication filed on 5/3/2000 is not fully responsive to the communication mailed 4/11/2000 for the reason(s) set forth on the attached Notice to Comply With the Sequence Rules or CRF Diskette Problem Report.

Since the response appears to be bona fide, but through an apparent oversight or inadvertence failed to provide a complete response, applicant is given **ONE (1) MONTH or THIRTY (30) DAYS** from the mailing date of this notice, whichever is longer, within which to supply the omission or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication should be directed to Examiner Ron Schwadron, Ph.D., Art Unit 1644, whose telephone number is 703-308-4680.

Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is (703) 308-0196.

RONALD B. SCHWADRON
PRIMARY EXAMINER
GROUP 1800-1644

Ron Schwadron, Ph.D.
Art Unit 1644

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

1644

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/155,514A

DATE: 05/18/2000

TIME: 07:15:09

Input Set : A:\1102_98.app

Output Set: N:\CRF3\05182000\I155514.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Kainoh, Mie
 4 Tanaka, Toshiaki
 5 <120> TITLE OF INVENTION: Chimeric proteins, their heterodimer complexes, and platelet
 6 substitutes
 7 <130> FILE REFERENCE: 1102-98
 8
 9
 9 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00370
 10 <151> PRIOR FILING DATE: 1997-01-29
 11 <150> PRIOR APPLICATION NUMBER: JP 9-15118
 12 <151> PRIOR FILING DATE: 1997-01-29
 13 <150> PRIOR APPLICATION NUMBER: JP 9-234544
 14 <151> PRIOR FILING DATE: 1997-08-29
 15 <160> NUMBER OF SEQ ID: 34
 16 <170> SOFTWARE: Microsoft Word 2000

ERRORED SEQUENCES

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 32 ggc ccc gaa gct gca ctc cgg gag acg gtg atg ctg ttg ctg tgc ctg 96
 33 Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Leu Cys Leu
 34 -20 -15 -10
 35 ggg gtc ccg acc ggc agg cct tac aac gtg gac act gag agc gcg ctg 144
 36 Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu
 37 -5 1 5
 38 ctt tac cag ggc ccc cac aac acg ctg ttc ggc tac tcg gtc gtg ctg 192
 39 Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu
 40 10 15 20 25
 41 cac agc cac ggg gcg aac cga tgg ctc cta gtg ggt gcg ccc act gcc 240
 42 His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala
 43 30 35 40
 44 aac tgg ctc gcc aac gct tca gtg atc aat ccc ggg gcg att tac aga 288
 45 Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg
 46 45 50 55
 47 tgc acg atc gga aag aat ccc ggc cag acg tgc gaa cag ctc cag ctg 336

RAW SEQUENCE LISTING

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51 Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Glu Arg
52          75          80          85
55 gac aat cag tgg ttg ggg gtc aca ctt tcc aga cag cca gga gaa aat 432
56 Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn
57 90          95          100          105
58 gga tcc atc gtg act tgt ggg cat aga tgg aaa aat ata ttt tac ata 480
59 Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile
60          110          115          120
61 aag aat gaa aat aag ctc ccc act ggt ggt tgc tat gga gtg ccc cct 528
62 Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro
63          125          130          135
64 gat tta cga aca gaa ctg agt aaa aga ata gct ccg tgt tat caa gat 576
65 Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp
66          140          145          150
67 tat gtg aaa aaa ttt gga gaa aat ttt gca tca tgt caa gct gga ata 624
68 Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile
69          155          160          165
70 tcc agt ttt tac aca aag gat tta att gtg atg ggg gcc cca gga tca 672
71 Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser
72 170          175          180          185
73 tct tac tgg act ggc tct ctt ttt gtc tac aat ata act aca aat aaa 720
74 Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys
75          190          195          200
76 tac aag gct ttt tta gac aaa caa aat caa gta aaa ttt gga agt tat 768
77 Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr
78          205          210          215
79 tta gga tat tca gtc gga gct ggt cat ttt cgg agc cag cat act acc 816
80 Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr
81          220          225          230
82 gaa gta gtc gga gga gct cct caa cat gag cag att ggt aag gca tat 864
83 Glu Val Val Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys Ala Tyr
84          235          240          245
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86 Ile Phe Ser Ile Asp Glu Lys Glu Leu Asn Ile Leu His Glu Met Lys
87 250          255          260          265
88 ggt aaa aag ctt gga tgc tac ttt gga gct tct gtc tgt gct gtg gac 960
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90          270          275          280
91 ctc aat gca gat ggc ttc tca gat ctg ctc gtg gga gca ccc atg cag 1008
92 Leu Asn Ala Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Gln
93          285          290          295
94 agc acc atc aga gag gaa gga aga gtg ttt gtg tac atc aac tct ggc 1056
95 Ser Thr Ile Arg Glu Glu Gly Arg Val Phe Val Tyr Ile Asn Ser Gly
96          300          305          310
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98 Ser Gly Ala Val Met Asn Ala Met Glu Thr Asn Leu Val Gly Ser Asp

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TIME: 07:15:09

Input Set : A:\1102_98.app

Output Set: N:\CRF3\05182000\I155514.raw

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200 Ile Lys Ala Asp Pro His Cys Leu Asn Phe Leu Cys Asn Phe Gly Lys
201      860      865      870
202 atg gaa agt gga aaa gaa gcc agt gtt cat atc caa ctg gaa ggc cgg 2784
203 Met Glu Ser Gly Lys Glu Ala Ser Val His Ile Gln Leu Glu Gly Arg
204      875      880      885
205 cca tcc att tta gaa atg gat gag act tca gca ctc aag ttt gaa ata 2832
206 Pro Ser Ile Leu Glu Met Asp Glu Thr Ser Ala Leu Lys Phe Glu Ile
207 890      895      900      905
208 aga gca aca ggt ttt cca gag cca aat cca aga gta att gaa cta aac 2880
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211 aag gat gag aat gtt gcg cat gtt cta ctg gaa gga cta cat cat caa 2928
212 Lys Asp Glu Asn Val Ala His Val Leu Leu Glu Gly Leu His His Gln
213      925      930      935
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215 Arg Pro Lys Arg Tyr Phe Thr Asp Pro Glu
216      940      945
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222 ctcccagatt ccagtaactc ccaatcttct ctctgca gag ccc aaa tct tgt gac 3333
223      Glu Pro Lys Ser Cys Asp
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226 Lys Thr His Thr Cys Pro Pro Cys Pro
227      955      960
228 gccctccagc tcaaggcggg acagggtgcc tagagtagcc tgcattccagg gacaggcccc 3440
229 agccgggtgc tgacacgtcc acctccatct ctctctca gca cct gaa ctc ctg 3493
230      Ala Pro Glu Leu Leu
231      965
232 ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc 3541
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236 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
237      985      990      995
238 cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag 3637
239 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
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241 gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg 3685
242 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
243      1020      1025      1030
244 tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat 3733
245 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

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246          1035          1040          1045
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250 atc gag aaa acc atc tcc aaa gcc aaa ggtgggaccc gtggggtgcg 3828
251 Ile Glu Lys Thr Ile Ser Lys Ala Lys
252          1065          1070
253 agggccacat ggacagaggc cggctcggcc caccctctgc cctgagagtg accgctgtac 3888
255 caacctctgt cctaca ggg cag ccc cga gaa cca cag gtg tac acc ctg 3937
256          Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
257          1075          1080
258 ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc 3985
259 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
260          1085          1090          1095
261 ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc 4033
262 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
263 1100          1105          1110          1115
264 aat ggg cag cgg gag aac aac tac aag acc acg cct ccc gtg ctg gat 4081
265 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Pro Pro Val Leu Asp
266          1120          1125          1130
267 tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc 4129
268 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
269          1135          1140          1145
271 agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct 4177
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273          1150          1155          1160
274 ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa 4225
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673 tta gcg ctc agt caa ggc att tta aat tgt tgt ttg gcc tac aat gtt 96
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675          -10          -5          1
E--> 676 ggt ctc cca gaa gca aaa ata ttt tcc ggt cct tca agt gaa cag ttt 114 144
677 Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe
678          5          10          15
679 ggg tat gca gtg cag cag ttt ata aat cca aaa ggc aac tgg tta ctg 192

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JUN - 8 2000

TC 1500 MAIL ROOM

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/155,514A

DATE: 05/18/2000

TIME: 07:15:09

Input Set : A:\1102_98.app

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682	ggt	ggt	tca	ccc	tgg	agt	ggc	ttt	cct	gag	aac	cga	atg	gga	gat	gtg	240
683	Val	Gly	Ser	Pro	Trp	Ser	Gly	Phe	Pro	Glu	Asn	Arg	Met	Gly	Asp	Val	
684				40						45					50		
685	tat	aaa	tgt	cct	ggt	gac	cta	tcc	act	gcc	aca	tgt	gaa	aaa	cta	aat	288
686	Tyr	Lys	Cys	Pro	Val	Asp	Leu	Ser	Thr	Ala	Thr	Cys	Glu	Lys	Leu	Asn	
687				55					60					65			
688	ttg	caa	act	tca	aca	agc	att	cca	aat	ggt	act	gag	atg	aaa	acc	aac	336
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691	atg	agc	ctc	ggc	ttg	atc	ctc	acc	agg	aac	atg	gga	act	gga	ggt	ttt	384
692	Met	Ser	Leu	Gly	Leu	Ile	Leu	Thr	Arg	Asn	Met	Gly	Thr	Gly	Gly	Phe	
693		85				90					95						
694	ctc	aca	tgt	ggt	cct	ctg	tgg	gca	cag	caa	tgt	ggg	aat	cag	tat	tac	432
695	Leu	Thr	Cys	Gly	Pro	Leu	Trp	Ala	Gln	Gln	Cys	Gly	Asn	Gln	Tyr	Tyr	
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702			135					140					145				
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704	Val	Val	Cys	Asp	Glu	Ser	Asn	Ser	Ile	Tyr	Pro	Trp	Asp	Ala	Val	Lys	
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707	Asn	Phe	Leu	Glu	Lys	Phe	Val	Gln	Gly	Leu	Asp	Ile	Gly	Pro	Thr	Lys	
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710	Thr	Gln	Val	Gly	Leu	Ile	Gln	Tyr	Ala	Asn	Asn	Pro	Arg	Val	Val	Phe	
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712	aac	ttg	aac	aca	tat	aaa	acc	aaa	gaa	gaa	atg	att	gta	gca	aca	tcc	720
713	Asn	Leu	Asn	Thr	Tyr	Lys	Thr	Lys	Glu	Glu	Met	Ile	Val	Ala	Thr	Ser	
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715	cag	aca	tcc	caa	tat	ggt	ggg	gac	ctc	aca	aac	aca	ttc	gga	gca	att	768
716	Gln	Thr	Ser	Gln	Tyr	Gly	Gly	Asp	Leu	Thr	Asn	Thr	Phe	Gly	Ala	Ile	
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719	Gln	Tyr	Ala	Arg	Lys	Tyr	Ala	Tyr	Ser	Ala	Ala	Ser	Gly	Gly	Arg	Arg	
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721	agt	gct	acg	aaa	gta	atg	gta	ggt	gta	act	gac	ggt	gaa	tca	cat	gat	864
722	Ser	Ala	Thr	Lys	Val	Met	Val	Val	Val	Thr	Asp	Gly	Glu	Ser	His	Asp	
723		245				250					255						
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725	Gly	Ser	Met	Leu	Lys	Ala	Val	Ile	Asp	Gln	Cys	Asn	His	Asp	Asn	Ile	
726	260				265						270				275		
727	ctg	agg	ttt	ggc	ata	gca	ggt	ctt	ggg	tac	tta	aac	aga	aac	gcc	ctt	960
728	Leu	Arg	Phe	Gly	Ile	Ala	Val	Leu	Gly	Tyr	Leu	Asn	Arg	Asn	Ala	Leu	

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734 Thr Glu Arg Tyr Phe Phe Asn Val Ser Asp Glu Ala Ala Leu Leu Glu
735          310          315          320
736 aag gct ggg aca tta gga gaa caa att ttc agc att gaa ggt act gtt 1104
737 Lys Ala Gly Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val
738          325          330          335
739 caa gga gga gac aac ttt cag atg gaa atg tca caa gtg gga ttc agt 1152
740 Gln Gly Gly Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser
741          340          345          350          355
742 gca gat tac tct tct caa aat gat att ctg atg ctg ggt gca gtg gga 1200
743 Ala Asp Tyr Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly
744          360          365          370
745 gct ttt ggc tgg agt ggg acc att gtc cag aag aca tct cat ggc cat 1248
746 Ala Phe Gly Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His
747          375          380          385
748 ttg atc ttt cct aaa caa gcc ttt gac caa att ctg cag gac aga aat 1296
749 Leu Ile Phe Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn
750          390          395          400
751 cac agt tca tat tta ggt tac tct gtg gct gca att tct act gga gaa 1344
752 His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu
753          405          410          415
754 agc act cac ttt gtt gct ggt gct cct cgg gca aat tat acc ggc cag 1392
755 Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln
756          420          425          430          435
757 ata gtg cta tat agt gtg aat gag aat ggc aat atc acg gtt att cag 1440
758 Ile Val Leu Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln
759          440          445          450
760 gct cac cga ggt gac cag att ggc tcc tat ttt ggt agt gtg ctg tgt 1488
761 Ala His Arg Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys
762          455          460          465
763 tca gtt gat gtg gat aaa gac acc att aca gac gtg ctc ttg gta ggt 1536
764 Ser Val Asp Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly
765          470          475          480
766 gca cca atg tac atg agt gac cta aag aaa gag gaa gga aga gtc tac 1584
767 Ala Pro Met Tyr Met Ser Asp Leu Lys Lys Glu Glu Gly Arg Val Tyr
768          485          490          495
769 ctg ttt act atc aaa aag ggc att ttg ggt cag cac caa ttt ctt gaa 1632
770 Leu Phe Thr Ile Lys Lys Gly Ile Leu Gly Gln His Gln Phe Leu Glu
771          500          505          510          515
772 ggc ccc gag ggc att gaa aac act cga ttt ggt tca gca att gca gct 1680
773 Gly Pro Glu Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala
774          520          525          530
775 ctt tca gac atc aac atg gat ggc ttt aat gat gtg att gtt ggt tca 1728
776 Leu Ser Asp Ile Asn Met Asp Gly Phe Asn Asp Val Ile Val Gly Ser
777          535          540          545

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/155,514A

DATE: 05/18/2000

TIME: 07:15:09

Input Set : A:\1102_98.app

Output Set: N:\CRF3\05182000\I155514.raw

```

778 cca cta gaa aat cag aat tct gga gct gta tac att tac aat ggt cat 1776
779 Pro Leu Glu Asn Gln Asn Ser Gly Ala Val Tyr Ile Tyr Asn Gly His
780      550      555      560
781 cag ggc act atc cgc aca aag tat tcc cag aaa atc ttg gga tcc gat 1824
782 Gln Gly Thr Ile Arg Thr Lys Tyr Ser Gln Lys Ile Leu Gly Ser Asp
783      565      570      575
784 gga gcc ttt agg agc cat ctc cag tac ttt ggg agg tcc ttg gat ggc 1872
785 Gly Ala Phe Arg Ser His Leu Gln Tyr Phe Gly Arg Ser Leu Asp Gly
786      580      585      590      595
787 tat gga gat tta aat ggg gat tcc atc acc gat gtg tct att ggt gcc 1920
788 Tyr Gly Asp Leu Asn Gly Asp Ser Ile Thr Asp Val Ser Ile Gly Ala
789      600      605      610
790 ttt gga caa gtg gtt caa ctc tgg tca caa agt att gct gat gta gct 1968
791 Phe Gly Gln Val Val Gln Leu Trp Ser Gln Ser Ile Ala Asp Val Ala
792      615      620      625
793 ata gaa gct tca ttc aca cca gaa aaa atc act ttg gtc aac aag aat 2016
794 Ile Glu Ala Ser Phe Thr Pro Glu Lys Ile Thr Leu Val Asn Lys Asn
795      630      635      640
796 gct cag ata att ctc aaa ctc tgc ttc agt gca aag ttc aga cct act 2064
797 Ala Gln Ile Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr
798      645      650      655
799 aag caa aac aat caa gtg gcc att gta tat aac atc aca ctt gat gca 2112
800 Lys Gln Asn Asn Gln Val Ala Ile Val Tyr Asn Ile Thr Leu Asp Ala
801      660      665      670      675
802 gat gga ttt tca tcc aga gta acc tcc agg ggg tta ttt aaa gaa aac 2160
803 Asp Gly Phe Ser Ser Arg Val Thr Ser Arg Gly Leu Phe Lys Glu Asn
804      680      685      690
805 aat gaa agg tgc ctg cag aag aat atg gta gta aat caa gca cag agt 2208
806 Asn Glu Arg Cys Leu Gln Lys Asn Met Val Val Asn Gln Ala Gln Ser
807      695      700      705
808 tgc ccc gag cac atc att tat ata cag gag ccc tct gat gtt gtc aac 2256
809 Cys Pro Glu His Ile Ile Tyr Ile Gln Glu Pro Ser Asp Val Val Asn
810      710      715      720
811 tct ttg gat ttg cgt gtg gac atc agt ctg gaa aac cct ggc act agc 2304
812 Ser Leu Asp Leu Arg Val Asp Ile Ser Leu Glu Asn Pro Gly Thr Ser
813      725      730      735
814 cct gcc ctt gaa gcc tat tct gag act gcc aag gtc ttc agt att cct 2352
815 Pro Ala Leu Glu Ala Tyr Ser Glu Thr Ala Lys Val Phe Ser Ile Pro
816      740      745      750      755
817 ttc cac aaa gac tgt ggt gag gat gga ctt tgc att tct gat cta gtc 2400
818 Phe His Lys Asp Cys Gly Glu Asp Gly Leu Cys Ile Ser Asp Leu Val
819      760      765      770
820 cta gat gtc cga caa ata cca gct gct caa gaa caa ccc ttt att gtc 2448
821 Leu Asp Val Arg Gln Ile Pro Ala Ala Gln Glu Gln Pro Phe Ile Val
822      775      780      785
823 agc aac caa aac aaa agg tta aca ttt tca gta aca ctg aaa aat aaa 2496
824 Ser Asn Gln Asn Lys Arg Leu Thr Phe Ser Val Thr Leu Lys Asn Lys
825      790      795      800
826 agg gaa agt gca tac aac act gga att gtt gtt gat ttt tca gaa aac 2544

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RAW SEQUENCE LISTING

DATE: 05/18/2000

PATENT APPLICATION: US/09/155,514A

TIME: 07:15:09

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Output Set: N:\CRF3\05182000\I155514.raw

827	Arg	Glu	Ser	Ala	Tyr	Asn	Thr	Gly	Ile	Val	Val	Asp	Phe	Ser	Glu	Asn	
828		805					810					815					
829	ttg	ttt	ttt	gca	tca	ttc	tcc	cta	ccg	gtt	gat	ggg	aca	gaa	gta	aca	2592
830	Leu	Phe	Phe	Ala	Ser	Phe	Ser	Leu	Pro	Val	Asp	Gly	Thr	Glu	Val	Thr	
831	820					825					830				835		
832	tgc	cag	gtg	gct	gca	tct	cag	aag	tct	gtt	gcc	tgc	gat	gta	ggc	tac	2640
833	Cys	Gln	Val	Ala	Ala	Ser	Gln	Lys	Ser	Val	Ala	Cys	Asp	Val	Gly	Tyr	
834				840						845				850			
835	cct	gct	tta	aag	aga	gaa	caa	cag	gtg	act	ttt	act	att	aac	ttt	gac	2688
836	Pro	Ala	Leu	Lys	Arg	Glu	Gln	Gln	Val	Thr	Phe	Thr	Ile	Asn	Phe	Asp	
837			855					860					865				
838	ttc	aat	ctt	caa	aac	ctt	cag	aat	cag	gcg	tct	ctc	agt	ttc	caa	gcc	2736
839	Phe	Asn	Leu	Gln	Asn	Leu	Gln	Asn	Gln	Ala	Ser	Leu	Ser	Phe	Gln	Ala	
840		870					875					880					
841	tta	agt	gaa	agc	caa	gaa	gaa	aac	aag	gct	gat	aat	ttg	gtc	aac	ctc	2784
842	Leu	Ser	Glu	Ser	Gln	Glu	Glu	Asn	Lys	Ala	Asp	Asn	Leu	Val	Asn	Leu	
843		885					890					895					
844	aaa	att	cct	ctc	ctg	tat	gat	gct	gaa	att	cac	tta	aca	aga	tct	acc	2832
845	Lys	Ile	Pro	Leu	Leu	Tyr	Asp	Ala	Glu	Ile	His	Leu	Thr	Arg	Ser	Thr	
846	900				905					910				915			
847	aac	ata	aat	ttt	tat	gaa	atc	tct	tcg	gat	ggg	aat	gtt	cct	tca	atc	2880
848	Asn	Ile	Asn	Phe	Tyr	Glu	Ile	Ser	Ser	Asp	Gly	Asn	Val	Pro	Ser	Ile	
849			920					925					930				
850	gtg	cac	agt	ttt	gaa	gat	gtt	ggt	cca	aaa	ttc	atc	ttc	tcc	ctg	aag	2928
851	Val	His	Ser	Phe	Glu	Asp	Val	Gly	Pro	Lys	Phe	Ile	Phe	Ser	Leu	Lys	
852			935					940				945					
853	gta	aca	aca	gga	agt	gtt	cca	gta	agc	atg	gca	act	gta	atc	atc	cac	2976
854	Val	Thr	Thr	Gly	Ser	Val	Pro	Val	Ser	Met	Ala	Thr	Val	Ile	Ile	His	
855		950					955					960					
856	atc	cct	cag	tat	acc	aaa	gaa	aag	aac	cca	ctg	atg	tac	cta	act	ggg	3024
857	Ile	Pro	Gln	Tyr	Thr	Lys	Glu	Lys	Asn	Pro	Leu	Met	Tyr	Leu	Thr	Gly	
858		965					970					975					
859	gtg	caa	aca	gac	aag	gct	ggt	gac	atc	agt	tgt	aat	gca	gat	atc	aat	3072
860	Val	Gln	Thr	Asp	Lys	Ala	Gly	Asp	Ile	Ser	Cys	Asn	Ala	Asp	Ile	Asn	
861	980				985						990			995			
862	cca	ctg	aaa	ata	gga	caa	aca	tct	tct	tct	gta	tct	ttc	aaa	agt	gaa	3120
863	Pro	Leu	Lys	Ile	Gly	Gln	Thr	Ser	Ser	Ser	Val	Ser	Phe	Lys	Ser	Glu	
864			1000					1005				1010					
865	aat	ttc	agg	cac	acc	aaa	gaa	ttg	aac	tgc	aga	act	gct	tcc	tgt	agt	3168
866	Asn	Phe	Arg	His	Thr	Lys	Glu	Leu	Asn	Cys	Arg	Thr	Ala	Ser	Cys	Ser	
867		1015					1020					1025					
868	aat	gtt	acc	tgc	tgg	ttg	aaa	gac	gtt	cac	atg	aaa	gga	gaa	tac	ttt	3216
869	Asn	Val	Thr	Cys	Trp	Leu	Lys	Asp	Val	His	Met	Lys	Gly	Glu	Tyr	Phe	
870		1030					1035				1040						
871	gtt	aat	gtg	act	acc	aga	att	tgg	aac	ggg	act	ttc	gca	tca	tca	acg	3264
872	Val	Asn	Val	Thr	Thr	Arg	Ile	Trp	Asn	Gly	Thr	Phe	Ala	Ser	Ser	Thr	
873		1045				1050					1055						
874	ttc	cag	aca	gta	cag	cta	acg	gca	gct	gca	gaa	atc	aac	acc	tat	aac	3312
875	Phe	Gln	Thr	Val	Gln	Leu	Thr	Ala	Ala	Ala	Glu	Ile	Asn	Thr	Tyr	Asn	

RAW SEQUENCE LISTING

DATE: 05/18/2000

PATENT APPLICATION: US/09/155,514A

TIME: 07:15:09

Input Set : A:\1102_98.app

Output Set: N:\CRF3\05182000\I155514.raw

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876 1060          1065          1070          1075
877 cct gag ata tat gtg att gaa gat aac act gtt acg att ccc ctg atg 3360
878 Pro Glu Ile Tyr Val Ile Glu Asp Asn Thr Val Thr Ile Pro Leu Met
879          1080          1085          1090
880 ata atg aaa cct gat gag aaa gcc gaa gta cca aca gat ccc gag 3405
881 Ile Met Lys Pro Asp Glu Lys Ala Glu Val Pro Thr Asp Pro Glu
882          1095          1100          1105
883 ctgctggaag caggtctcagc gctcctgcct ggaagcatcc cggctatgca gccccagtcc 3465
884 agggcagcaa ggcaggcccc gtctgcctct tcaccgggag cctotgccc cccactcat 3525
885 gctcaggag agggctctct ggccttttcc caggctctgg gcaggcacag gctagggtgcc 3585
886 cctaaccag gccctgcaca caaaggggca ggtgctgggc tcagacctgc caagagccat 3645
887 atccgggagg accctgcccc tgacctaaag ccacccaaa ggcctaaactc tccactccct 3705
888 cagctcggac acctctctc ctccagatt ccagtaactc ccaatcttct ctctgca 3762
889 gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca 3807
890 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
891          1110          1115          1120
892 ggtaagccag ccaggcctc gccctccagc tcaaggcggg acaggtgccc tagagtagcc 3867
893 tgcattccagg gacaggcccc agccgggtgc tgacacgtcc acctccatct ctctctca 3925
894 gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa 3973
895 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
896          1125          1130          1135
897 ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg 4021
898 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
899          1140          1145          1150
900 gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac 4069
901 Val Val Asp Val Ser His Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
902          1155          1160          1165
904 gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag 4117
905 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
906 1170          1175          1180          1185
907 cag tac aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac 4165
908 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
909          1190          1195          1200
910 cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa 4213
911 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
912          1205          1210          1215
913 gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa 4255
914 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
915          1220          1225          1230
916 ggtgggaccc gtgggtgctg agggccacat ggacagaggc cggctcggcc caccctctgc 4315
917 cctgagagtg accgctgtac caacctctgt cctaca ggg cag ccc cga gaa cca 4369
918          Gly Gln Pro Arg Glu Pro
919          1235
920 cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag 4417
921 Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
922          1240          1245          1250
923 gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc 4465
924 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
925          1255          1260          1265

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/155,514A

DATE: 05/18/2000

TIME: 07:15:09

Input Set : A:\1102_98.app

Output Set: N:\CRF3\05182000\I155514.raw

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926 gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg 4513
927 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
928 1270 1275 1280 1285
929 cct ccc gtg ctg gat tcc gac ggc tcc ttc ttc ctc tac agc aag ctc 4561
930 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
931 1290 1295 1300
932 acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc 4609
933 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
934 1305 1310 1315
935 gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc 4657
936 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
937 1320 1325 1330
938 ctg tct ccg ggt aaa tga 4675
939 Leu Ser Pro Gly Lys
940 1335
1077 <210> SEQ ID NO: 32
1078 <211> LENGTH: 1179
1079 <212> TYPE: PRT
1080 <213> ORGANISM: Homo sapien
1082 <400> SEQUENCE: 32
1083 Met Phe Pro Thr Glu Ser Ala Trp Leu Gly Lys Arg Gly Ala Asn Pro
1084 -35 -30 -25
1086 Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Leu Cys Leu
1087 -20 -15 -10
1089 Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu
1090 -5 1 5
1092 Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu
1093 10 15 20 25
1095 His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala
1096 30 35 40
1098 Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg
1099 45 50 55
1101 Cys Arg Ile Gly Lys Asn Pro Gly Gln Thr Cys Glu Gln Leu Gln Leu
1102 60 65 70
1104 Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Glu Arg
1105 75 80 85
1107 Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn
1108 90 95 100 105
1110 Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile
1111 110 115 120
1113 Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro
1114 125 130 135
1116 Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp
1117 140 145 150
1119 Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile
1120 155 160 165
1122 Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser
1123 170 175 180 185
1125 Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys

```

1218 (p. 15) (please include negative numbers in
 <211> response)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/155,514A

DATE: 05/18/2000

TIME: 07:15:09

Input Set : A:\1102_98.app

Output Set: N:\CRF3\05182000\I155514.raw

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1126          190          195          200
1128 Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr
1129          205          210          215
1131 Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr
1132          220          225          230
1135 Glu Val Val Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys Ala Tyr
1136          235          240          245
1138 Ile Phe Ser Ile Asp Glu Lys Glu Leu Asn Ile Leu His Glu Met Lys
1139 250          255          260          265
1141 Gly Lys Lys Leu Gly Ser Tyr Phe Gly Ala Ser Val Cys Ala Val Asp
1142          270          275          280
1144 Leu Asn Ala Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Gln
1145          285          290          295
1147 Ser Thr Ile Arg Glu Glu Gly Arg Val Phe Val Tyr Ile Asn Ser Gly
1148          300          305          310
1150 Ser Gly Ala Val Met Asn Ala Met Glu Thr Asn Leu Val Gly Ser Asp
1151          315          320          325
1153 Lys Tyr Ala Ala Arg Phe Gly Glu Ser Ile Val Asn Leu Gly Asp Ile
1154 330          335          340          345
1156 Asp Asn Asp Gly Phe Glu Asp Val Ala Ile Gly Ala Pro Gln Glu Asp
1157          350          355          360
1159 Asp Leu Gln Gly Ala Ile Tyr Ile Tyr Asn Gly Arg Ala Asp Gly Ile
1160          365          370          375
1162 Ser Ser Thr Phe Ser Gln Arg Ile Glu Gly Leu Gln Ile Ser Lys Ser
1163          380          385          390
1165 Leu Ser Met Phe Gly Gln Ser Ile Ser Gly Gln Ile Asp Ala Asp Asn
1166          395          400          405
1168 Asn Gly Tyr Val Asp Val Ala Val Gly Ala Phe Arg Ser Asp Ser Ala
1169 410          415          420          425
1171 Val Leu Leu Arg Thr Arg Pro Val Val Ile Val Asp Ala Ser Leu Ser
1172          430          435          440
1174 His Pro Glu Ser Val Asn Arg Thr Lys Phe Asp Cys Val Glu Asn Gly
1175          445          450          455
1177 Trp Pro Ser Val Cys Ile Asp Leu Thr Leu Cys Phe Ser Tyr Lys Gly
1178          460          465          470
1180 Lys Glu Val Pro Gly Tyr Ile Val Leu Phe Tyr Asn Met Ser Leu Asp
1181          475          480          485
1183 Val Asn Arg Lys Ala Glu Ser Pro Pro Arg Phe Tyr Phe Ser Ser Asn
1184 490          495          500          505
1186 Gly Thr Ser Asp Val Ile Thr Gly Ser Ile Gln Val Ser Ser Arg Glu
1187          510          515          520
1189 Ala Asn Cys Arg Thr His Gln Ala Phe Met Arg Lys Asp Val Arg Asp
1190          525          530          535
1192 Ile Leu Thr Pro Ile Gln Ile Glu Ala Ala Tyr His Leu Gly Pro His
1193          540          545          550
1195 Val Ile Ser Lys Arg Ser Thr Glu Glu Phe Pro Pro Leu Gln Pro Ile
1196          555          560          565
1198 Leu Gln Gln Lys Lys Glu Lys Asp Ile Met Lys Lys Thr Ile Asn Phe
1199 570          575          580          585

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/155,514A

DATE: 05/18/2000

TIME: 07:15:09

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Output Set: N:\CRF3\05182000\I155514.raw

```

1201 Ala Arg Phe Cys Ala His Glu Asn Cys Ser Ala Asp Leu Gln Val Ser
1202                               590                               595                               600
1204 Ala Lys Ile Gly Phe Leu Lys Pro His Glu Asn Lys Thr Tyr Leu Ala
1205                               605                               610                               615
1207 Val Gly Ser Met Lys Thr Leu Met Leu Asn Val Ser Leu Phe Asn Ala
1208                               620                               625                               630
1210 Gly Asp Asp Ala Tyr Glu Thr Thr Leu His Val Lys Leu Pro Val Gly
1211                               635                               640                               645
1213 Leu Tyr Phe Ile Lys Ile Leu Glu Leu Glu Lys Gln Ile Asn Cys
1214 650                               655                               660                               665
1216 Glu Val Thr Asp Asn Ser Gly Val Val Gln Leu Asp Cys Ser Ile Gly
1217                               670                               675                               680
1219 Tyr Ile Tyr Val Asp His Leu Ser Arg Ile Asp Ile Ser Phe Leu Leu
1220                               685                               690                               695
1222 Asp Val Ser Ser Leu Ser Arg Ala Glu Glu Asp Leu Ser Ile Thr Val
1223                               700                               705                               710
1225 His Ala Thr Cys Glu Asn Glu Glu Glu Met Asp Asn Leu Lys His Ser
1226                               715                               720                               725
1228 Arg Val Thr Val Ala Ile Pro Leu Lys Tyr Glu Val Lys Leu Thr Val
1229 730                               735                               740                               745
1231 His Gly Phe Val Asn Pro Thr Ser Phe Val Tyr Gly Ser Asn Asp Glu
1232                               750                               755                               760
1234 Asn Glu Pro Glu Thr Cys Met Val Glu Lys Met Asn Leu Thr Phe His
1235                               765                               770                               775
1237 Val Ile Asn Thr Gly Asn Ser Met Ala Pro Asn Val Ser Val Glu Ile
1238                               780                               785                               790
1240 Met Val Pro Asn Ser Phe Ser Pro Gln Thr Asp Lys Leu Phe Asn Ile
1241                               795                               800                               805
1243 Leu Asp Val Gln Thr Thr Thr Gly Glu Cys His Phe Glu Asn Tyr Gln
1244 810                               815                               820                               825
1246 Arg Val Cys Ala Leu Glu Gln Gln Lys Ser Ala Met Gln Thr Leu Lys
1247                               830                               835                               840
1249 Gly Ile Val Arg Phe Leu Ser Lys Thr Asp Lys Arg Leu Leu Tyr Cys
1250                               845                               850                               855
1252 Ile Lys Ala Asp Pro His Cys Leu Asn Phe Leu Cys Asn Phe Gly Lys
1253                               860                               865                               870
1255 Met Glu Ser Gly Lys Glu Ala Ser Val His Ile Gln Leu Glu Gly Arg
1256                               875                               880                               885
1258 Pro Ser Ile Leu Glu Met Asp Glu Thr Ser Ala Leu Lys Phe Glu Ile
1259 890                               895                               900                               905
1261 Arg Ala Thr Gly Phe Pro Glu Pro Asn Pro Arg Val Ile Glu Leu Asn
1262                               910                               915                               920
1264 Lys Asp Glu Asn Val Ala His Val Leu Glu Glu Gly Leu His His Gln
1265                               925                               930                               935
1267 Arg Pro Lys Arg Tyr Phe Thr Asp Pro Glu Glu Pro Lys Ser Cys Asp
1268                               940                               945                               950
1270 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
1271                               955                               960                               965
1273 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/155,514A

DATE: 05/18/2000

TIME: 07:15:09

Input Set : A:\1102_98.app

Output Set: N:\CRF3\05182000\I155514.raw

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1274 970          975          980          985
1276 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
1277          990          995          1000
1279 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
1280          1005          1010          1015
1282 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
1283          1020          1025          1030
1285 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
1286          1035          1040          1045
1288 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
1289 1050          1055          1060          1065
1291 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
1292          1070          1075          1080
1294 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
1295          1085          1090          1095
1297 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
1298          1100          1105          1110
1300 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
1301          1115          1120          1125
1303 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
1304 1130          1135          1140          1145
1306 Lys Ser Arg Trp Gln Gly Asn Val Phe Ser Cys Ser Val Met His
1307          1150          1155          1160
1309 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
1310          1165          1170          1175
E--> 1312 Gly Lys
1315 <210> SEQ ID NO: 33
1316 <211> LENGTH: 943
1317 <212> TYPE: PRT
1318 <213> ORGANISM: Homo sapien
1320 <400> SEQUENCE: 33
1323 Met Asn Leu Gln Pro Ile Phe Trp Ile Gly Leu Ile Ser Ser Val Cys
1324 -20          -15          -10          -5
1326 Cys Val Phe Ala Gln Thr Asp Glu Asn Arg Cys Leu Lys Ala Asn Ala
1327          1          5          10
1329 Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys
1330          15          20          25
1332 Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys
1333          30          35          40
1335 Asp Asp Leu Glu Ala Leu Lys Lys Lys Gly Cys Pro Pro Asp Asp Ile
1336 45          50          55          60
1338 Glu Asn Pro Arg Gly Ser Lys Asp Ile Lys Lys Asn Lys Asn Val Thr
1339          65          70          75
1341 Asn Arg Ser Lys Gly Thr Ala Glu Lys Leu Lys Pro Glu Asp Ile His
1342          80          85          90
1344 Gln Ile Gln Pro Gln Gln Leu Val Leu Arg Leu Arg Ser Gly Glu Pro
1345          95          100          105
1347 Gln Thr Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp
1348          110          115          120

```

963(p.18)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/155,514A

DATE: 05/18/2000

TIME: 07:15:09

Input Set : A:\1102_98.app

Output Set : N:\CRF3\05182000\I155514.raw

```

1351 Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Glu
1352 125 130 135 140
1354 Asn Val Lys Ser Leu Gly Thr Asp Leu Met Asn Glu Met Arg Arg Ile
1355 145 150 155
1357 Thr Ser Asp Phe Arg Ile Gly Phe Gly Ser Phe Val Glu Lys Thr Val
1358 160 165 170
1360 Met Pro Tyr Ile Ser Thr Thr Pro Ala Lys Leu Arg Asn Pro Cys Thr
1361 175 180 185
1363 Ser Glu Gln Asn Cys Thr Thr Pro Phe Ser Tyr Lys Asn Val Leu Ser
1364 190 195 200
1366 Leu Thr Asn Lys Gly Glu Val Phe Asn Glu Leu Val Gly Lys Gln Arg
1367 205 210 215 220
1369 Ile Ser Gly Asn Leu Asp Ser Pro Glu Gly Gly Phe Asp Ala Ile Met
1370 225 230 235
1372 Gln Val Ala Val Cys Gly Ser Leu Ile Gly Trp Arg Asn Val Thr Arg
1373 240 245 250
1375 Leu Leu Val Phe Ser Thr Asp Ala Gly Phe His Phe Ala Gly Asp Gly
1376 255 260 265
1378 Lys Leu Gly Gly Ile Val Leu Pro Asn Asp Gly Gln Cys His Leu Glu
1379 270 275 280
1381 Asn Asn Met Tyr Thr Met Ser His Tyr Tyr Asp Tyr Pro Ser Ile Ala
1382 285 290 295 300
1384 His Leu Val Gln Lys Leu Ser Glu Asn Asn Ile Gln Thr Ile Phe Ala
1385 305 310 315
1387 Val Thr Glu Glu Phe Gln Pro Val Tyr Lys Glu Leu Lys Asn Leu Ile
1388 320 325 330
1390 Pro Lys Ser Ala Val Gly Thr Leu Ser Ala Asn Ser Ser Asn Val Ile
1391 335 340 345
1393 Gln Leu Ile Ile Asp Ala Tyr Asn Ser Leu Ser Ser Glu Val Ile Leu
1394 350 355 360
1396 Glu Asn Gly Lys Leu Ser Glu Gly Val Thr Ile Ser Tyr Lys Ser Tyr
1397 365 370 375 380
1399 Cys Lys Asn Gly Val Asn Gly Thr Gly Glu Asn Gly Arg Lys Cys Ser
1400 385 390 395
1402 Asn Ile Ser Ile Gly Asp Glu Val Gln Phe Glu Ile Ser Ile Thr Ser
1403 400 405 410
1405 Asn Lys Cys Pro Lys Lys Asp Ser Asp Ser Phe Lys Ile Arg Pro Leu
1406 415 420 425
1408 Gly Phe Thr Glu Glu Val Glu Val Ile Leu Gln Tyr Ile Cys Glu Cys
1409 430 435 440
1411 Glu Cys Gln Ser Glu Gly Ile Pro Glu Ser Pro Lys Cys His Glu Gly
1412 445 450 455 460
1414 Asn Gly Thr Phe Glu Cys Gly Ala Cys Arg Cys Asn Glu Gly Arg Val
1415 465 470 475
1417 Gly Arg His Cys Glu Cys Ser Thr Asp Glu Val Asn Ser Glu Asp Met
1418 480 485 490
1420 Asp Ala Tyr Cys Arg Lys Glu Asn Ser Ser Glu Ile Cys Ser Asn Asn
1421 495 500 505
1423 Gly Glu Cys Val Cys Gly Gln Cys Val Cys Arg Lys Arg Asp Asn Thr

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/155,514A

DATE: 05/18/2000

TIME: 07:15:09

Input Set : A:\1102_98.app

Output Set: N:\CRF3\05182000\I155514.raw

```

1424      510                      515                      520
1426 Asn Glu Ile Tyr Ser Gly Lys Phe Cys Glu Cys Asp Asn Phe Asn Cys
1427 525                      530                      535                      540
1429 Asp Arg Ser Asn Gly Leu Ile Cys Gly Gly Asn Gly Val Cys Lys Cys
1430                      545                      550                      555
1432 Arg Val Cys Glu Cys Asn Pro Asn Tyr Thr Gly Ser Ala Cys Asp Cys
1433                      560                      565                      570
1435 Ser Leu Asp Thr Ser Thr Cys Glu Ala Ser Asn Gly Gln Ile Cys Asn
1436                      575                      580                      585
1438 Gly Arg Gly Ile Cys Glu Cys Gly Val Cys Lys Cys Thr Asp Pro Lys
1439 590                      595                      600
1441 Phe Gln Gly Gln Thr Cys Glu Met Cys Gln Thr Cys Leu Gly Val Cys
1442 605                      610                      615                      620
1444 Ala Glu His Lys Glu Cys Val Gln Cys Arg Ala Phe Asn Lys Gly Glu
1445                      625                      630                      635
1447 Lys Lys Asp Thr Cys Thr Gln Glu Cys Ser Tyr Phe Asn Ile Thr Lys
1448                      640                      645                      650
1450 Val Glu Ser Arg Asp Lys Leu Pro Gln Pro Val Gln Pro Asp Pro Val
1451                      655                      660                      665
1453 Ser His Cys Lys Glu Lys Asp Val Asp Asp Cys Trp Phe Tyr Phe Thr
1454 670                      675                      680
1456 Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn
1457 685                      690                      695                      700
1459 Pro Glu Cys Pro Thr Gly Pro Glu Asp Pro Glu Glu Pro Lys Ser Cys
1460                      705                      710                      715
1462 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1463                      720                      725                      730
1465 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
1466                      735                      740                      745
1468 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
1469 750                      755                      760
1471 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
1472 765                      770                      775                      780
1474 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
1475                      785                      790                      795
1477 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
1478                      800                      805                      810
1480 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
1481                      815                      820                      825
1483 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
1484 830                      835                      840
1486 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
1487 845                      850                      855                      860
1489 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
1490                      865                      870                      875
1492 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
1493                      880                      885                      890
1495 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
1496                      895                      900                      905

```

RAW SEQUENCE LISTING

DATE: 05/18/2000

PATENT APPLICATION: US/09/155,514A

TIME: 07:15:09

Input Set : A:\1102_98.app

Output Set: N:\CRF3\05182000\I155514.raw

1498 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 1499 910 915 920
 1501 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 1502 925 930 935 940
 E--> 1504 Pro Gly Lys
 1506 <210> SEQ ID NO: 34
 1507 <211> LENGTH: 1338
 1508 <212> TYPE: PRT
 1509 <213> ORGANISM: Homo sapien
 W--> 1510 <300> PUBLICATION INFORMATION:
 1512 <400> SEQUENCE: 34
 1513 Met Gly Pro Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Val
 1514 -25 -20 -15
 1516 Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val
 1517 -10 -5 1
 1519 Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe
 1520 5 10 15
 1522 Gly Tyr Ala Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu
 1523 20 25 30 35
 1525 Val Gly Ser Pro Trp Ser Gly Phe Pro Glu Asn Arg Met Gly Asp Val
 1526 40 45 50
 1528 Tyr Lys Cys Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn
 1529 55 60 65
 1531 Leu Gln Thr Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn
 1532 70 75 80
 1534 Met Ser Leu Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Gly Phe
 1535 85 90 95
 1537 Leu Thr Cys Gly Pro Leu Trp Ala Gln Gln Cys Gly Asn Gln Tyr Tyr
 1538 100 105 110 115
 1540 Thr Thr Gly Val Cys Ser Asp Ile Ser Pro Asp Phe Gln Leu Ser Ala
 1541 120 125 130
 1543 Ser Phe Ser Pro Ala Thr Gln Pro Cys Pro Ser Leu Ile Asp Val Val
 1544 135 140 145
 1546 Val Val Cys Asp Glu Ser Asn Ser Ile Tyr Pro Trp Asp Ala Val Lys
 1547 150 155 160
 1549 Asn Phe Leu Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys
 1550 165 170 175
 1552 Thr Gln Val Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Val Val Phe
 1553 180 185 190 195
 1555 Asn Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser
 1556 200 205 210
 1558 Gln Thr Ser Gln Tyr Gly Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile
 1559 215 220 225
 1561 Gln Tyr Ala Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg
 1562 230 235 240
 1564 Ser Ala Thr Lys Val Met Val Val Val Thr Asp Gly Glu Ser His Asp
 1565 245 250 255
 1567 Gly Ser Met Leu Lys Ala Val Ile Asp Gln Cys Asn His Asp Asn Ile
 1568 260 265 270 275

RAW SEQUENCE LISTING

DATE: 05/18/2000

PATENT APPLICATION: US/09/155,514A

TIME: 07:15:09

Input Set : A:\1102_98.app

Output Set: N:\CRF3\05182000\I155514.raw

```

1570 Leu Arg Phe Gly Ile Ala Val Leu Gly Tyr Leu Asn Arg Asn Ala Leu
1571                280                285                290
1573 Asp Thr Lys Asn Leu Ile Lys Glu Ile Lys Ala Ile Ala Ser Ile Pro
1574                295                300                305
1576 Thr Glu Arg Tyr Phe Phe Asn Val Ser Asp Glu Ala Ala Leu Leu Glu
1577                310                315                320
1579 Lys Ala Gly Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val
1580                325                330                335
1582 Gln Gly Gly Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser
1583 340                345                350                355
1585 Ala Asp Tyr Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly
1586                360                365                370
1588 Ala Phe Gly Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His
1589                375                380                385
1591 Leu Ile Phe Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn
1592                390                395                400
1594 His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu
1595                405                410                415
1597 Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln
1598 420                425                430                435
1600 Ile Val Leu Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln
1601                440                445                450
1603 Ala His Arg Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys
1604                455                460                465
1606 Ser Val Asp Val Asp Lys Asp Thr Ile Thr Asp Val Leu Val Gly
1607                470                475                480
1609 Ala Pro Met Tyr Met Ser Asp Leu Lys Lys Glu Glu Gly Arg Val Tyr
1610                485                490                495
1612 Leu Phe Thr Ile Lys Lys Gly Ile Leu Gly Gln His Gln Phe Leu Glu
1613 500                505                510                515
1615 Gly Pro Glu Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala
1616                520                525                530
1618 Leu Ser Asp Ile Asn Met Asp Gly Phe Asn Asp Val Ile Val Gly Ser
1619                535                540                545
1621 Pro Leu Glu Asn Gln Asn Ser Gly Ala Val Tyr Ile Tyr Asn Gly His
1622                550                555                560
1624 Gln Gly Thr Ile Arg Thr Lys Tyr Ser Gln Lys Ile Leu Gly Ser Asp
1625                565                570                575
1627 Gly Ala Phe Arg Ser His Leu Gln Tyr Phe Gly Arg Ser Leu Asp Gly
1628 580                585                590                595
1630 Tyr Gly Asp Leu Asn Gly Asp Ser Ile Thr Asp Val Ser Ile Gly Ala
1631                600                605                610
1633 Phe Gly Gln Val Val Gln Leu Trp Ser Gln Ser Ile Ala Asp Val Ala
1634                615                620                625
1636 Ile Glu Ala Ser Phe Thr Pro Glu Lys Ile Thr Leu Val Asn Lys Asn
1637                630                635                640
1639 Ala Gln Ile Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr
1640                645                650                655
1642 Lys Gln Asn Asn Gln Val Ala Ile Val Tyr Asn Ile Thr Leu Asp Ala

```

RAW SEQUENCE LISTING

DATE: 05/18/2000

PATENT APPLICATION: US/09/155,514A

TIME: 07:15:09

Input Set : A:\1102_98.app

Output Set: N:\CRF3\05182000\I155514.raw

```

1643 660          665          670          675
1645 Asp Gly Phe Ser Ser Arg Val Thr Ser Arg Gly Leu Phe Lys Glu Asn
1646          680          685          690
1648 Asn Glu Arg Cys Leu Gln Lys Asn Met Val Val Asn Gln Ala Gln Ser
1649          695          700          705
1651 Cys Pro Glu His Ile Ile Tyr Ile Gln Glu Pro Ser Asp Val Val Asn
1652          710          715          720
1654 Ser Leu Asp Leu Arg Val Asp Ile Ser Leu Glu Asn Pro Gly Thr Ser
1655          725          730          735
1657 Pro Ala Leu Glu Ala Tyr Ser Glu Thr Ala Lys Val Phe Ser Ile Pro
1658 740          745          750          755
1660 Phe His Lys Asp Cys Gly Glu Asp Gly Leu Cys Ile Ser Asp Leu Val
1661          760          765          770
1663 Leu Asp Val Arg Gln Ile Pro Ala Ala Gln Glu Gln Pro Phe Ile Val
1664          775          780          785
1666 Ser Asn Gln Asn Lys Arg Leu Thr Phe Ser Val Thr Leu Lys Asn Lys
1667          790          795          800
1669 Arg Glu Ser Ala Tyr Asn Thr Gly Ile Val Val Asp Phe Ser Glu Asn
1670          805          810          815
1672 Leu Phe Phe Ala Ser Phe Ser Leu Pro Val Asp Gly Thr Glu Val Thr
1673 820          825          830          835
1675 Cys Gln Val Ala Ala Ser Gln Lys Ser Val Ala Cys Asp Val Gly Tyr
1676          840          845          850
1678 Pro Ala Leu Lys Arg Glu Gln Gln Val Thr Phe Thr Ile Asn Phe Asp
1679          855          860          865
1681 Phe Asn Leu Gln Asn Leu Gln Asn Gln Ala Ser Leu Ser Phe Gln Ala
1682          870          875          880
1684 Leu Ser Glu Ser Gln Glu Glu Asn Lys Ala Asp Asn Leu Val Asn Leu
1685          885          890          895
1687 Lys Ile Pro Leu Leu Tyr Asp Ala Glu Ile His Leu Thr Arg Ser Thr
1688 900          905          910          915
1690 Asn Ile Asn Phe Tyr Glu Ile Ser Ser Asp Gly Asn Val Pro Ser Ile
1691          920          925          930
1693 Val His Ser Phe Glu Asp Val Gly Pro Lys Phe Ile Phe Ser Leu Lys
1694          935          940          945
1696 Val Thr Thr Gly Ser Val Pro Val Ser Met Ala Thr Val Ile Ile His
1697          950          955          960
1699 Ile Pro Gln Tyr Thr Lys Glu Lys Asn Pro Leu Met Tyr Leu Thr Gly
1700          965          970          975
1702 Val Gln Thr Asp Lys Ala Gly Asp Ile Ser Cys Asn Ala Asp Ile Asn
1703 980          985          990          995
1705 Pro Leu Lys Ile Gly Gln Thr Ser Ser Ser Val Ser Phe Lys Ser Glu
1706          1000          1005          1010
1708 Asn Phe Arg His Thr Lys Glu Leu Asn Cys Arg Thr Ala Ser Cys Ser
1709          1015          1020          1025
1711 Asn Val Thr Cys Trp Leu Lys Asp Val His Met Lys Gly Glu Tyr Phe
1712          1030          1035          1040
1714 Val Asn Val Thr Thr Arg Ile Trp Asn Gly Thr Phe Ala Ser Ser Thr
1715          1045          1050          1055

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/155,514A

DATE: 05/18/2000

TIME: 07:15:09

Input Set : A:\1102_98.app

Output Set: N:\CRF3\05182000\I155514.raw

```

1717 Phe Gln Thr Val Gln Leu Thr Ala Ala Ala Glu Ile Asn Thr Tyr Asn
1718 1060                      1065                      1070                      1075
1720 Pro Glu Ile Tyr Val Ile Glu Asp Asn Thr Val Thr Ile Pro Leu Met
1721                      1080                      1085                      1090
1723 Ile Met Lys Pro Asp Glu Lys Ala Glu Val Pro Thr Asp Pro Glu Glu
1724                      1095                      1100                      1105
1726 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
1727                      1110                      1115                      1120
1729 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
1730                      1125                      1130                      1135
1732 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
1733 1140                      1145                      1150                      1155
1735 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
1736                      1160                      1165                      1170
1738 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
1739                      1175                      1180                      1185
1741 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
1742                      1190                      1195                      1200
1744 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
1745                      1205                      1210                      1215
1747 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
1748 1220                      1225                      1230                      1235
1750 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
1751                      1240                      1245                      1250
1753 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
1754                      1255                      1260                      1265
1756 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
1757                      1270                      1275                      1280
1759 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
1760                      1285                      1290                      1295
1762 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
1763 1300                      1305                      1310                      1315
1765 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
1766                      1320                      1325                      1330
1768 Leu Ser Leu Ser Pro Gly Lys
E--> 1769                      1335

```

VERIFICATION SUMMARY

DATE: 05/18/2000

PATENT APPLICATION: US/09/155,514A

TIME: 07:15:10

Input Set : A:\1102_98.app

Output Set: N:\CRF3\05182000\I155514.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier
L:7 M:283 W: Missing Blank Line separator, <130> field identifier
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:283 W: Missing Blank Line separator, <160> field identifier
L:22 M:283 W: Missing Blank Line separator, <220> field identifier
L:25 M:283 W: Missing Blank Line separator, <300> field identifier
L:187 M:254 E: (42) Number of Bases conflicts Running Total, LENGTH:Input:2588 Counted:2544
L:284 M:283 W: Missing Blank Line separator, <220> field identifier
L:287 M:283 W: Missing Blank Line separator, <300> field identifier
L:288 M:283 W: Missing Blank Line separator, <400> field identifier
L:496 M:283 W: Missing Blank Line separator, <220> field identifier
L:496 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:508 M:283 W: Missing Blank Line separator, <220> field identifier
L:509 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:511 M:283 W: Missing Blank Line separator, <400> field identifier
L:518 M:283 W: Missing Blank Line separator, <220> field identifier
L:519 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:521 M:283 W: Missing Blank Line separator, <400> field identifier
L:528 M:283 W: Missing Blank Line separator, <220> field identifier
L:529 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:531 M:283 W: Missing Blank Line separator, <400> field identifier
L:539 M:283 W: Missing Blank Line separator, <220> field identifier
L:540 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:552 M:283 W: Missing Blank Line separator, <220> field identifier
L:553 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:555 M:283 W: Missing Blank Line separator, <400> field identifier
L:562 M:283 W: Missing Blank Line separator, <220> field identifier
L:563 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:565 M:283 W: Missing Blank Line separator, <400> field identifier
L:572 M:283 W: Missing Blank Line separator, <220> field identifier
L:573 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:575 M:283 W: Missing Blank Line separator, <400> field identifier
L:582 M:283 W: Missing Blank Line separator, <220> field identifier
L:583 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:585 M:283 W: Missing Blank Line separator, <400> field identifier
L:592 M:283 W: Missing Blank Line separator, <220> field identifier
L:593 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:595 M:283 W: Missing Blank Line separator, <400> field identifier
L:602 M:283 W: Missing Blank Line separator, <220> field identifier
L:603 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:605 M:283 W: Missing Blank Line separator, <400> field identifier
L:612 M:283 W: Missing Blank Line separator, <220> field identifier
L:613 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:615 M:283 W: Missing Blank Line separator, <400> field identifier
L:622 M:283 W: Missing Blank Line separator, <220> field identifier
L:623 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:625 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/155,514A

DATE: 05/18/2000

TIME: 07:15:10

Input Set : A:\1102_98.app

Output Set: N:\CRF3\05182000\I155514.raw

L:632 M:283 W: Missing Blank Line separator, <220> field identifier
L:632 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:635 M:283 W: Missing Blank Line separator, <400> field identifier
L:643 M:283 W: Missing Blank Line separator, <220> field identifier
L:643 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:646 M:283 W: Missing Blank Line separator, <400> field identifier
L:654 M:283 W: Missing Blank Line separator, <220> field identifier
L:654 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:657 M:283 W: Missing Blank Line separator, <400> field identifier
L:665 M:283 W: Missing Blank Line separator, <220> field identifier
L:668 M:283 W: Missing Blank Line separator, <300> field identifier
L:669 M:283 W: Missing Blank Line separator, <400> field identifier
L:676 M:254 E: (42) Number of Bases conflicts Running Total, LENGTH:Input:114 Counted:144
L:946 M:283 W: Missing Blank Line separator, <220> field identifier
L:947 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:949 M:283 W: Missing Blank Line separator, <400> field identifier
L:956 M:283 W: Missing Blank Line separator, <220> field identifier
L:957 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:959 M:283 W: Missing Blank Line separator, <400> field identifier
L:967 M:283 W: Missing Blank Line separator, <220> field identifier
L:968 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:970 M:283 W: Missing Blank Line separator, <400> field identifier
L:977 M:283 W: Missing Blank Line separator, <220> field identifier
L:978 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:980 M:283 W: Missing Blank Line separator, <400> field identifier
L:987 M:283 W: Missing Blank Line separator, <220> field identifier
L:987 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:999 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1010 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1021 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1032 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1043 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1054 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1066 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1312 M:252 E: (20) Calc# of Seq. differs from actual, <211> LENGTH:Input:1179 Counted:1218
L:1504 M:252 E: (20) Calc# of Seq. differs from actual, <211> LENGTH:Input:943 Counted:963
L:1769 M:252 E: (20) Calc# of Seq. differs from actual, <211> LENGTH:Input:1338 Counted:1367